

Figure 1

1 GATTOGGCACGAGAACTTTTAAATCTTTAGTTATTTCTTAATACTTAGAACACTTAAAC 60

61 AAAACTTTACAAAACAAAAGAGCAGAATAATTAGATCCTTTTACAGAGAAATGACTTTTTT 120

121 TTTCCTAAGCACACTGGACCATAGAGGAAGACCAAGGAATGTACAGTTGCTGCTCCTT 180
1 M Y S C L L L 7

181 CCTGACTTGCTGTATTGTACTCTGCCCCACTGGTGGTGGCAATGCTATTAAACCCACAC 240
8 P D L L Y L T L S P L V V A M L L T P H 27

241 TTTAACGTGGCAAATCCCAGAATCTGTTGGCTGGTCTCTGGCTAGAGAATGAGCACAGT 300
28 F N V A N P Q N L L A G L W L E N E H S 47

301 TTCACCCTTATGGCTCCAGAAAGAGCAAGAACACACCACTGCCAGCCAGAAGAGAGAAAA 360
48 F T L M A P E R A R T H H C Q P E E R K 67

361 GTCTTGTTCTGTCTCTTTCCATTGTCCCAAATAGCCAAGCACAGGTTCAACCACCCCAA 420
68 V L F C L F P I V P N S Q A Q V Q P P Q 87

421 ATGCCACCCTTCTGCTGTGCAGCAGCCAAGGAAAAGACCCAGGAGGAGCAGCTCCAAGAA 480
88 M P P F C C A A A K E K T Q E E Q L Q E 107

481 CCTCTGGGCAGTCAGTGCCAGATACTTGCCCCAATTCTTTGTGTCCAAGCCACACTCAG 540
108 P L G S Q C P D T C P N S L C P S H T Q 127

541 CTGACAAAAGCCAACACTTTGTCTCTCTTTTCTTTTCTTTTCTTTTCTTTTGTAGCAGAGTT 600
128 L T K A N T L S L F F F F S F F L S R V 147

601 TCACCTTTGTCAACCAGGCTGGAGTGCATGgCAGGATCTTGGCTCATTGCAACTCCAC 660
148 S L L S P R L E C N G R I L A H C N L H 167

661 CtCCCGGGTTCAAGCAATCTCCTGTCTCAGCCTCTCGA 699
168 L P G S S N S P V S A S R 180

Figure 2

